SEQUENCE LISTING

SEQ ID NO:1 - FVO-PCR1;

5'-GGGTCGGTACCATGGCAGTAACTCCTTCCGTAATTGAT-3'

SEQ ID NO:2 - FVO-PCR2;

5'-GGATCAGATGCGGCCGCTTAACTGCAGAAAATACCATCGAAAAGTGGA-3'

SEQ ID NO:3 - EA3;

5'-TAAAAAATATATAAACGACAAAC-3'

SEQ ID NO:4 - EA5;

5'-AAAAGGGAAGATATTTCTCATTT-3'

SEQ ID NO:5 - EA485-CDFVO,

5'- CGCAGTTACTCCATCTGTTATTGATAATATTCTTTCTAAAATTGAAAACGAATATGAGGTTTTATATTTAA-3'

SEQ ID NO:6 - EA493-CDFVO,

5'-GGTTTTAAATATAAAACCTCATATTCGTTTTCAATTTTAGAAAGAATATTATCAATAACAGATGGAGTAACTGCGGTAC-3'

Table 1. Harmonization of *P. falciparum* MSP1-42 for expression in *E. coli* using *P. falciparum* and *E.coli* codon harmonization data

Residue	AA	Native Codon (P. falciparum)	Relat. Codon Usage (% dev from mean)	Harmonized codon (E coli cl. 2)	Relat. Codon Usage (% dev from mean)
1	A	GCA	71	GCT	10
2	V	GTA	65	GTT	59
3	T	ACT	4	ACG	-50
4	P	CCT	59	CCA	-39
5	S	TCC	-52	TCG	-56
6	V	GTA	65	GTT	59
7	I	ATT	18	ATT	2
8	D	GAT	73	GAC	8
9	N	AAC	-72	AAT	-65
10	I	ATA	65	ATC	100
11	L	CTT	-32	CTC	-50
12	S	TCT	39	AGC	46
13	K	AAA	63	AAA	57
14	I	ATT	18	ATT	2
15	E	GAA	71	GAA	51
16	N	AAT	72	AAC	65
17	E	GAA	71	GAA	51
18	Y	TAT	78	TAC	30
19	E	GAG	-71	GAG	-51
20	V	GTT	61	GTT	59
21	L	TTA	276	CTG	359
22	Y	TAT	78	TAC	30
23	L	TTA	276	CTG	359
24	K	AAA	63	AAA	57
25	P	CCT	59	CCA	-39
26	L	TTA	276	CTG	359
27	A	GCA	71	GCT	10
28	G	GGT	67	GGC	71
29	V	GTT	61	GTT	59
30	Y	TAT	78	TAC	30
31	R	AGA	263	CGT	285
32	S	AGT	91	TCT	94
33	L	TTA	276	CTG	359
34	K	AAA	63	AAA	57
35	K	AAA	63	AAA	57
36	Q	CAA	74	CAG	63
37	L	TTA	276	CTG	359
38	E	GAA	71	GAA	51
39	N	AAT	72	AAC	65
40	N	AAC	-72	AAT	-65
41	V	GTT	61	GTT	59
42	M	ATG	0	ATG	0
43	T	ACA	112	ACC	114
44	F	TTT	67	TTC	42

45	N	AAT	72	AAC	65
46	V	GTT	61	GTT	59
47	N	AAT	72	AAC	65
48	V	GTT	61	GTT	59
49	K	AAG	-63	AAG	-57
50	D	GAT	73	GAC	8
51	I	ATT	18	ATT	2
52	L	TTA	276	CTG	359
53	N	AAT	72	AAC	65
54	S	TCA	56	AGC	46
55	R	CGA	-46	CGC	98
56	F	TTT	67	TTC	42
57	N	AAT	72	AAC	65
58	K	AAA	63	AAA	57
59	R	CGT	-32	CGC	98
60	E	GAA	71	GAA	51
61	N	AAT	72	AAC	65
62	F	TTC	-67	TTC	-42
63	K	AAA	63	AAA	57
64	N	AAT	72	AAC	65
65	V	GTT	61	GTT	59
66	L	TTA	276	CTG	359
67	E	GAA	71	GAA	51
68	S	TCA	56	AGC	46
69	D	GAT	73	GAC	8
70	L	TTA	276	CTG	359
77	I	ATT	18	ATT	2
72	P	CCA	83	CCA	-39
73	Y	TAT	78	TAC	30
74	K	AAA	63	AAA	57
75	D	GAT	73	GAC	8
76	L	TTA	276	CTG	359
77	T	ACA	112	ACC	114
78	S	TCA	56	AGC	46
79	S	AGT	91	TCT	94
80	N	AAT	72	AAC	65
81	Y	TAT	78	TAC	30
82	V	GTT	61	GTT	59
83	V	GTC	-75	GTC	-46
84	K	AAA	63	AAA	57
85	D	GAT	73	GAC	8
86	P	CCA	83	CCA	-39
87	Y	TAT	78	TAC	30
88	K	AAA	63	AAA	57
89	F	TTT	67	TTC	42
90	L	CTT	-32	CTC	-50
91	N	AAT	72	AAC	65
92	K	AAA	63	AAA	57
93	E	GAA	71	GAA	51
94	K	AAA	63	AAA	57
95	R	AGA	263	CGT	285
96	D	GAT	73	GAC	8

97	K	AAA	63	AAA	57
98	F	TTC	-67	TTC	-42
99	L	TTA	276	CTG	359
100	S	AGC	-63	TCG	-56
101	S	AGT	91	TCT	94
102	Y	TAT	78	TAC	30
103	N	AAT	72	AAC	65
104	Y	TAT	78	TAC	30
105	I	ATT	18	ATT	2
106	K	AAG	-63	AAG	-57
107	D	GAT	73	GAC	8
108	S	TCA	56	AGC	46
109	I	ATA	65	ATC	100
110	D	GAT	73	GAC	8
111	T	ACG	-63	ACG	-50
112	D	GAT	73	GAC	8
113	I	ATA	65	ATC	100
114	N	AAT	72	AAC	65
115	F	TTT	67	TTC	42
116	A	GCA	71	GCT	10
117	N	AAT	72	AAC	65
118	D	GAT	73	GAC	8
119	V	GTT	61	GTT	59
120	L	CTT	-32	CTC	-50
121	G	GGA	107	GGC	71
122	Y	TAT	78	TAC	30
123	Y	TAT	78	TAC	30
124	K	AAA	63	AAA	57
125	I	ATA	65	ATC	100
126	L	TTA	276	CTG	359
127	S	TCC	-52	TCG	-56
128	E	GAG	-71	GAG	-51
129	K	AAA	63	AAA	57
130	Y	TAT	78	TAC	30
131	K	AAA	63	AGC	46
132	S	TCA	56	GAC	8
133	D	GAT	73	GAC	8
134	L	TTA	276	CTG	359
135	D	GAT	73	GAC	8
136	S	TCA	56	AGC	46
137	I	ATT	18	ATT	2
138	K	AAA	63	AAA	57
139	K	AAA	63	AAA	57
140	Y	TAT	78	TAC	30
141	I	ATA	65	ATC	100
142	N	AAC	-72	AAT	-65
143	D	GAC	-73	GAT	-8
144	K	AAA	63	AAA	57
145	Q	CAA	74	CAG	63
146	G	GGT	67	GGC	71
147	E	GAA	71	GAA	51
148	N	AAT	72	AAC	65

149	E	GAG	-71	GAG	-51
150	K	AAA	63	AAA	57
151	Y	TAC	-78	TAT	-30
152	L	CTT	-32	CTC	-50
153	P	CCC	-60	CCT	-55
154	F	TTT	67	TTC	42
155	L	TTA	276	CTG	359
156	N	AAC	-72	AAT	-65
157	N	AAT	72	AAC	65
158	I	ATT	18	ATT	2
159	E	GAG	-71	GAG	-51
160	T	ACC	-53	ACG	-50
161	L	TTA	276	CTG	359
162	Y	TAT	78	TAC	30
163	K	AAA	63	AAA	57
164	T	ACA	112	ACC	114
165	V	GTT	61	GTT	59
166	N	AAT	72	AAC	65
167	D	GAT	73	GAC	8
168	K	AAA	63	ATT	2
169	I	ATT	18	ATT	2
170	D	GAT	73	GAC	8
171	L	TTA	276	CTG	359
172	F	TTT	67	TTC	42
173	V	GTA	65	GTT	59
174	I	ATT	18	ATT	2
175	H	CAT	71	CAC	40
176	L	TTA	276	CTG	359
177	E	GAA	71	GAA	51
178	A	GCA	71	GCT	10
179	K	AAA	63	AAA	57
180	V	GTT	61	GTT	59
181	L	CTA	-52	CTC	-50
182	N	AAT	72	AAC	65
183	Y	TAT	78	TAC	30
184	T	ACA	112	ACC	114
185	Y	TAT	78	TAC	30
186	E	GAG	-71	GAG	-51
187	K	AAA	63	AAA	57
188	S	TCA	56	AGC	46
189	N	AAC	-72	AAT	-65
190	V	GTA	65	GTT	59
191	E	GAA	71	GAA	51
192	V	GTT	61	GTT	59
193	K	AAA	63	AAA	57
194	I	ATA	65	ATC	100
195	K	AAA	63	AAA	57
196	E	GAA	71	GAA	51
197	L	CTT	-32	CTC	-50
198	N	AAT	72	AAC	65
199	Y	TAC	-78	TAT	-30
200	L	TTA	276	CTG	359

201	K	AAA	63	AAA	57
202	T	ACA	112	ACC	114
203	I	ATT	18	ATT	2
204	Q	CAA	74	CAG	63
205	D	GAC	-73	GAT	-8
206	K	AAA	63	AAA	57
207	L	TTG	-18	CTC	-50
208	A	GCA	71	GCT	10
209	D	GAT	73	GAC	8
210	F	TTT	67	TTC	42
211	K	AAA	63	AAA	57
212	K	AAA	63	AAA	57
213	N	AAT	72	AAC	65
214	N	AAC	-72	AAT	-65
215	N	AAT	72	AAC	65
216	F	TTC	-67	TTC	-42
217	V	GTT	61	GTT	59
218	G	GGA	107	GGC	71
219	I	ATT	18	ATT	2
220	A	GCT	67	GCT	10
221	D	GAT	73	GAC	8
222	L	TTA	276	CTG	359
223	S	TCA	56	AGC	46
224	T	ACA	112	ACC	114
225	D	GAT	73	GAC	8
226	Y	TAT	78	TAC	30
227	N	AAC	-72	AAT	-65
228	H	CAT	71	CAC	40
229	N	AAT	72	AAC	65
230	N	AAC	-72	AAT	-65
231	L	TTA	276	CTG	359
232	L	TTG	-18	CTC	-50
233	T	ACA	112	ACC	114
234	K	AAG	-63	AAG	-57
235	F	TTC	-67	TTC	-42
236	L	CTT	-32	CTC	-50
237	S	AGT	91	TCT	94
238	T	ACA	112	ACC	114
239	G	GGT	67	GGC	71
240	M	ATG	0	ATG	0
241	V	GTT	61	GTT	59
242	F	TTT	67	TTC	42
243	E	GAA	71	GAA	51
244	N	AAT	72	AAC	65
245	L	CTC	-86	CTC	-50
246	A	GCT	67	GCT	10
247	K	AAA	63	AAA	57
248	T	ACC	-53	ACG	-50
249	V	GTT	61	GTT	59
250	L	TTA	276	CTG	359
251	S	TCT	39	AGC	46
252	N	AAT	72	AAC	65

253	L	TTA	276	CTG	359
254	L	CTT	-32	CTC	-50
255	D	GAT	73	GAC	8
256	G	GGA	107	GGC	71
257	N	AAC	-72	AAT	-65
258	L	TTG	-18	CTC	-50
259	Q	CAA	74	CAG	63
260	G	GGT	67	GGC	71
261	M	ATG	0	ATG	0
262	L	TTA	276	CTG	359
263	N	AAC	-72	AAT	-65
264	I	ATT	18	ATT	2
265	S	TCA	56	AGC	46
266	Q	CAA	74	CAG	63
267	H	CAC	-71	CAT	-40
268	Q	CAA	74	CAG	63
269	C	TGC	-75	TGT	-22
270	V	GTA	65	GTT	59
271	K	AAA	63	AAA	57
272	K	AAA	63	AAA	57
273	Q	CAA	74	CAG	63
274	C	TGT	75	TGC	22
275	P	CCA	83	CCA	-39
276	Q	CAA	74	CAG	63
277	N	AAT	72	AAC	65
278	S	TCT	39	AGC	46
279	G	GGA	107	GGC	71
280	C	TGT	75	TGC	22
281	F	TTC	-67	TTC	-42
282	R	AGA	263	CGT	285
283	H	CAT	71	CAC	40
284	L	TTA	276	CTG	359
285	D	GAT	73	GAC	8
286	E	GAA	71	GAA	51
287	R	AGA	263	CGT	285
288	E	GAA	71	GAA	51
289	E	GAA	71	GAA	51
290	C	TGT	75	TGC	22
291	K	AAA	63	AAA	57
292	C	TGT	75	TGC	22
293	L	TTA	276	CTG	359
294	L	TTA	276	CTG	359
295	N	AAT	72	AAC	65
296	Y	TAC	-78	TAT	-30
297	K	AAA	63	AAA	57
298	Q	CAA	74	CAG	63
299	E	GAA	71	GAA	51
300	G	GGT	67	GGC	71
301	D	GAT	73	GAC	8
302	K	AAA	63	AAA	57
303	C	TGT	75	TGC	22
304	V	GTT	61	GTT	59

305	E	GAA	71	GAA	51
306	N	AAT	72	AAC	65
307	P	CCA	83	CCA	-39
308	N	AAT	72	AAC	65
309	P	CCT	59	CCA	-39
310	T	ACT	4	ACG	-50
311	C	TGT	75	TGC	22
312	N	AAC	-72	AAT	-65
313	E	GAA	71	GAA	51
314	N	AAT	72	AAC	65
315	N	AAT	72	AAC	65
316	G	GGT	67	GGC	71
317	G	GGA	107	GGC	71
318	C	TGT	75	TGC	22
319	D	GAT	73	GAC	8
320	A	GCA	71	GCT	10
321	D	GAT	73	GAC	8
322	A	GCC	-58	GCC	-36
323	K	AAA	63	AAA	57
324	C	TGT	75	TGC	22
325	T	ACC	-53	ACG	-50
326	E	GAA	71	GAA	51
327	E	GAA	71	GAA	51
328	D	GAT	73	GAC	8
329	S	TCA	56	AGC	46
330	G	GGT	67	GGC	71
331	S	AGC	-63	TCG	-56
332	N	AAC	-72	AAT	-65
333	G	GGA	107	GGC	71
334	K	AAG	-63	AAG	-57
335	K	AAA	63	AAA	57
336	I	ATC	-80	ATT	19
337	T	ACA	112	ACC	114
338	C	TGT	75	TGC	22
339	E	GAA	71	GAA	51
340	C	TGT	75	TGC	22
341	T	ACT	4	ACG	-50
342	K	AAA	63	AAA	57
343	P	CCT	59	CCA	-39
344	D	GAT	73	GAC	8
345	S	TCT	39	AGC	46
346	Y	TAT	78	TAC	30
347	P	CCA	83	CCA	-39
348	L	CTT	-32	CTC	-50
349	F	TTC	-67	TTC	-42
350	D	GAT	73	GAC	8
351	G	GGT	67	GGC	71
352	I	ATT	18	ATT	2
353	F	TTC	-67	TTC	-42
354	C	TGC	-75	TGT	-22
355	S	AGT	91	AGT	-73

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